

FIGURE 1

1 ATGTCACTGGGACCCATGAAGAAGGGAGTGGGAGGGCAGTTGGCTTGGAGGGCGAGC  
 61 GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCAGACTGCCACTGGCTGGAGGGAGCTCCGGGACAA  
 121 EGTGGCAGGGCTGGAGGCTGCCAGGGCTGGCTGGAGGGAGCTCAGCTGGTGC  
 181 TGGGAGCAGGGGACCGGGACTGGCTGGATGGACCTGGAGCCCTCGCTGCTGCCACTGGT  
 241 CCCAATGCCAGCAACACCTCTGATGGCCCCGATAAACCTCACTTCAGGAGGATCACCTCTCCT  
 301 CGCACGGGGAGGCATCTCCTACATCAACATCATCATGCCTTCGGTGTGGCACCATCTGC  
 361 CTCCTGGGCATCATCGGGAACTCCACGGTCACTCTCGGGTCTGGTAAGAAGTCCAAGCTG  
 421 CACTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTGGTAGATGGGTGTGGCACTTT  
 481 TTTCCTGGCATGCCCTCATGATCCACCAAGCTCATGGCAATGGCAATGGGTGTGGCACTTT  
 541 GGGAGACCATGTGCACCCCTCATCACGGCCTACGGCATGGATGCCAATAGTCAGTTCAACAGCACC  
 601 TACATCCTGACCCGCATGGCCATTGACCCGCTACCTGGCCACTGTCCACCCCATCTCTTCC  
 661 ACGAAGTTCCGGAAAGCCCTGTGGCCACCTGGTGAATCTGCCCTCCTGGGCCCCCTCTCC  
 721 TTCAATCAGGCATCACCCCTGTGGCTGTATGCCAGACTCATCCCCCTTCAGGAGGTGCA  
 781 GTGGGCTGGGGCATAGGCCCTGCCAACCCAGACACTGACCTCTACTGGGTCAACCTGTAC  
 841 CAGTTTTCCCTGGCCTTGGCCTTGTGGTCAATCACAGCCGATACGTGAGGATC  
 901 CTGAGGGCATGACGTCCCTCAGTGGCCCCGGCTCCCAAGCGAGCATCGGGCTGGGACAA  
 961 AAGAGGGTGAACCGGACAGCCATGCCATCTGTCTGGCTTGTGCTGGGCCACCC  
 1021 TACTATGTGCTACAGCTGACCCAGTGTCCATCAGGGCCGACCTCACCTTGCTAC  
 1081 TTATACAATGCGGCCATCAGCTGGCTATGCCAACAGCTGCCCTAACCCCTTGTGTAC  
 1141 ATCGTGCTCTGTGAGAGCTGGCAAAACGCTGGTGGTGAAGCCCTGCAGGCCAG  
 1201 GGGCAGCTTCCGGCTGTCAAGAACGCTCAAGACGGCTGACGAGGAGGACAGAAAGCRAA  
 1261 GGCAACCTGA

FIGURE 2

1	M S V G A M K K G V G R A V G L G G G S	20
21	G C Q A T E E D P L P D C G A C A P G Q	40
41	G G R R W R L P Q P A W V E G S S A R L	60
61	W E Q A T G T G W M D L E A S L L P T G	80
81	P N A S N T S D G P D N L T S A G S P P	100
101	R T G S I S Y I N I I M P S V F G T I C	120
121	L L G I I G N S T V I F A V V K K S K L	140
141	H W C N N V P D I F I I N L S V V D L L	160
161	F L L G M P F M I H Q L M G N G V W H F	180
181	G E T M C T L I T A M D A N S Q F T S T	200
201	Y I L T A M A I D R Y L A T V H P I S S	220
221	T K F R K P S V A T L V I C L L W A L S	240
241	F I S I T P V W L Y A R L I P F P G G A	260
261	V G C G I R L P N P D T D L Y W F T L Y	280
281	Q F F L A F A L P F V V I T A A Y V R I	300
301	L Q R M T S S V A P A S Q R S I R L R T	320
321	K R V T R T A I A I C L V F F V C W A P	340
341	Y Y V L Q L T Q L S I S R P T L T F V Y	360
361	L Y N A A I S L G Y A N S C L N P F V Y	380
381	I V L C E T F R K R L V L S V K P A A Q	400
401	G Q L R A V S N A Q T A D E E R T E S K	420
421	G T	422

FIGURE 3

1 M S V G A M K K G V G R A V G L G G G S 20  
 21 G C Q A T E E D P L P D C G A C A P G Q 40  
 41 G G R R W R L P Q P A W V E G S S A R L 60  
 61 W E Q A T G T G W M D L E A S L L P T G 80  
 81 P N A S N T S D G P D N L T S A G S P P 100  
 101 R T G S I S Y I N IM P S V F G T I C 120  
 121 IL G I I G N S T V I F A V V K K S K L 140  
 141 H W C N N V P D I F I I N I S V V D L L 160  
 161 F L L G M P E M I H Q L M G N G V W H F 180  
 181 G E T M C T L I T A M D A N S O E T S T 200  
 201 T I I T A M A I D R Y L A T V H P I S S 220  
 221 T K F R K P S V A T L V I C I L L W A L S 240  
 241 F I S I T P V W I Y A R L I P F P G G A 260  
 261 V G C G I R L P N P D T D L Y W F T L Y 280  
 281 O F F L A F A I P F V V I T A A Y V R I 300  
 301 L Q R M T S S V A P A S Q R S I R L R T 320  
 321 K R V T P T A I A P I C L V F F V C W A P 340  
 341 V Y V L O L T O L S I S R P T L T F V Y 360  
 361 L Y N A A I S L G Y A N S C L N P F V Y 380  
 381 I V L C E T F R K R L V L S V K P A A Q 400  
 401 G Q L R A V S N A Q T A D E E R T E S K 420  
 421 G T 422

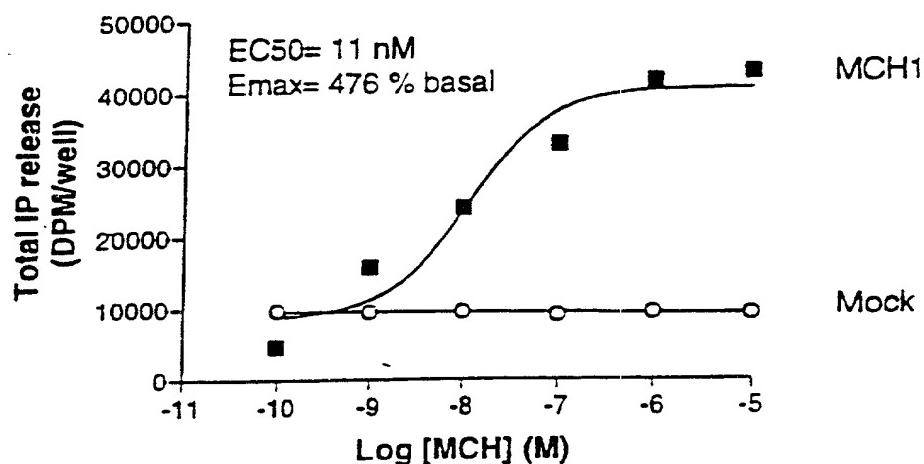
FIGURE 4

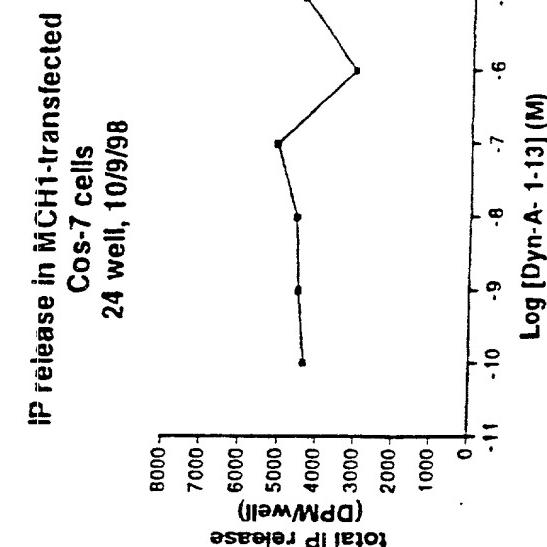
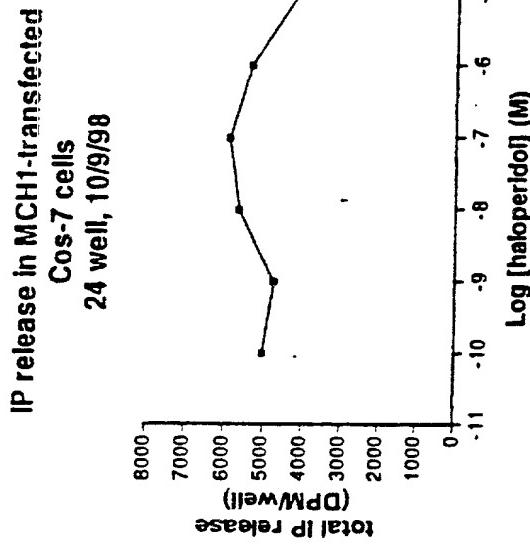
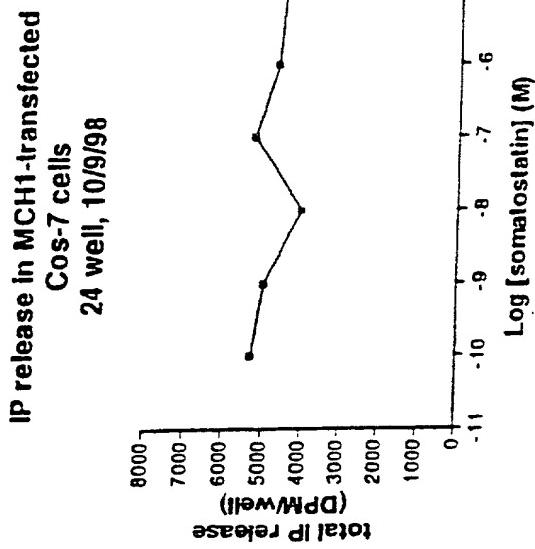
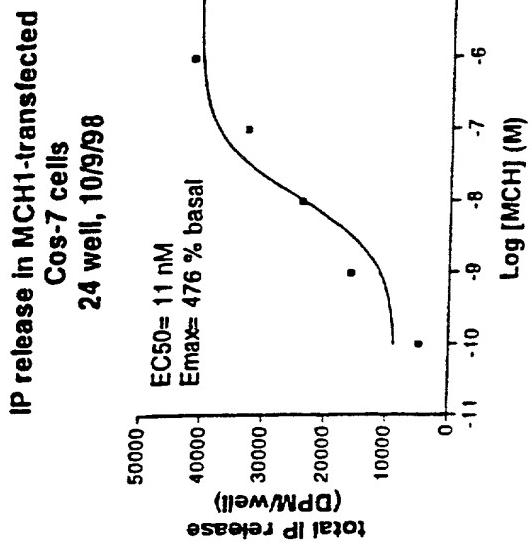
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 61    TGCCAGCAACATCTCCGATGGCCAGGATAAATCTCACATTGCGGGGTCAACCTCCTGCAC  
 121   AGGGAGTGTCTCTACATCAACATCATTATGCCCTCCCGTGTACCATCTGTCCT  
 181   GGGCATCGTGGAAACTCCACGGTCATCTTGTGGTAAGGAAGTCAAAGCTAACACTG  
 241   GTGCAAGCAACGTCGGGGACATCTCATCATCAACCTCTCTGTGGATCTGCTCTTCCT  
 301   GCTGGGCATGCGCTTTCATGATCCACCAAGCTCATGGGAACGGGGCTGGCACTTGGGA  
 361   AACCATGTCACCCCTCATCACAGGCCATGGACGCCAACAGTCAGTCACTAGCACCAT  
 421   CCTGACTGCCATGACCATTGACCGCTACTTGGCCACCCGTCACCCCATCTCCACCAA  
 481   GTTCCGGGAAGGCCCTCCATGGCCACCCCTGGTGAATCTGCCCTCCGGCTCTCCCTCAT  
 541   CAGTATCACCCCTGTGGCTCTACGCCAGGCTCATCCCTCCAGGGGTGCTGTGGG  
 601   CTGTGGCATCCGGCTGGCAAAACCCGGACACTGACCTCTACTGTTCACTGTACAGTT  
 661   TTTCCTGGCCTTGGCCCTTCCGTTGGTCAATTACCGCCGCAATACGTGAAAATACTACA  
 721   GGCATGACGTCTTCGGTGGCCAGGCTCCCAACCGAGCATCGGCTTGGACAAAGAG  
 781   GGTGCACCCGCACGGCCATTGCCATCTGTCGGCTCTGGTGTGGCACCCCTACTA  
 841   TGTGCTGCAGGTGACCCAGCTGTCCATCAGCCGGCCACGTTGTCTACTTGTGA  
 901   \* CAACGGGGCATCAGCTGGCTATGCTTACAGCTGGCTTGTGTACATAGT  
 961   GCTCTGTGAGACCTTCGAAACGCTGGTGTCACTGAAGGCCAGGGCA  
 1021   GCTCCGGCACGGTCAGCAACGCTAGACAGCTGATGAGGAGAGACGAAAGGCAC  
 1081   CTGACAATTCCCCAGTCGGCTCAAGTCAGGCCACCCATCAACCGTGGGGAGAGATA  
 1141   TGAGATTAACCCAAGGCTACCCCTGGGAGATGGAGGGCTGGGGCTTGTAG  
 1201   CAACCACATTCCAC

FIGURE 5

1	M D L Q T S L L S T G P N A S N I S D G	20
21	Q D N L Q T S L P G S T P R T G S V S Y I S T G	40
41	I I M P S V V F G T I C L L G I V G N S T I	60
61	V I F A V V K K S K L H W C S N V P D I	80
81	F I I N L S V V D L L F F L L G M P F M I T	100
101	H Q L M G N G V V W H F G E T M C T L I T D	120
121	A M D A N S Q F T S T K F R K P S M A L	140
141	R Y L A T V H P I S S F I S I T P V W L	160
161	T L V I C L L W A L S F I S I R L P N	180
181	Y A R L I P F P G G A Y Q F F L A F A L P	200
201	P D T D L Y W F F T L K Q R M T S S V A	220
221	F V V I T A A Y V T V K I L Q R V T R T A I A	240
241	P A S Q R S I R L R T K R V T R T Q L T Q	260
261	I C L V F F V C W A P Y Y V L Q L I S L G	280
281	S I S R P T L T F V Y I V L C E T F R K	300
301	Y A N S C L N P F V Y I V L R T V S N A	320
321	R L V L S V K P A A Q G Q T * R T V S N A	340
341	Q T A D E E R T E S K G G T * * 354	

FIGURE 6

**IP release in MCH1- and  
mock-transfected Cos-7 cells**



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FIGURE 7

FIGURE 8

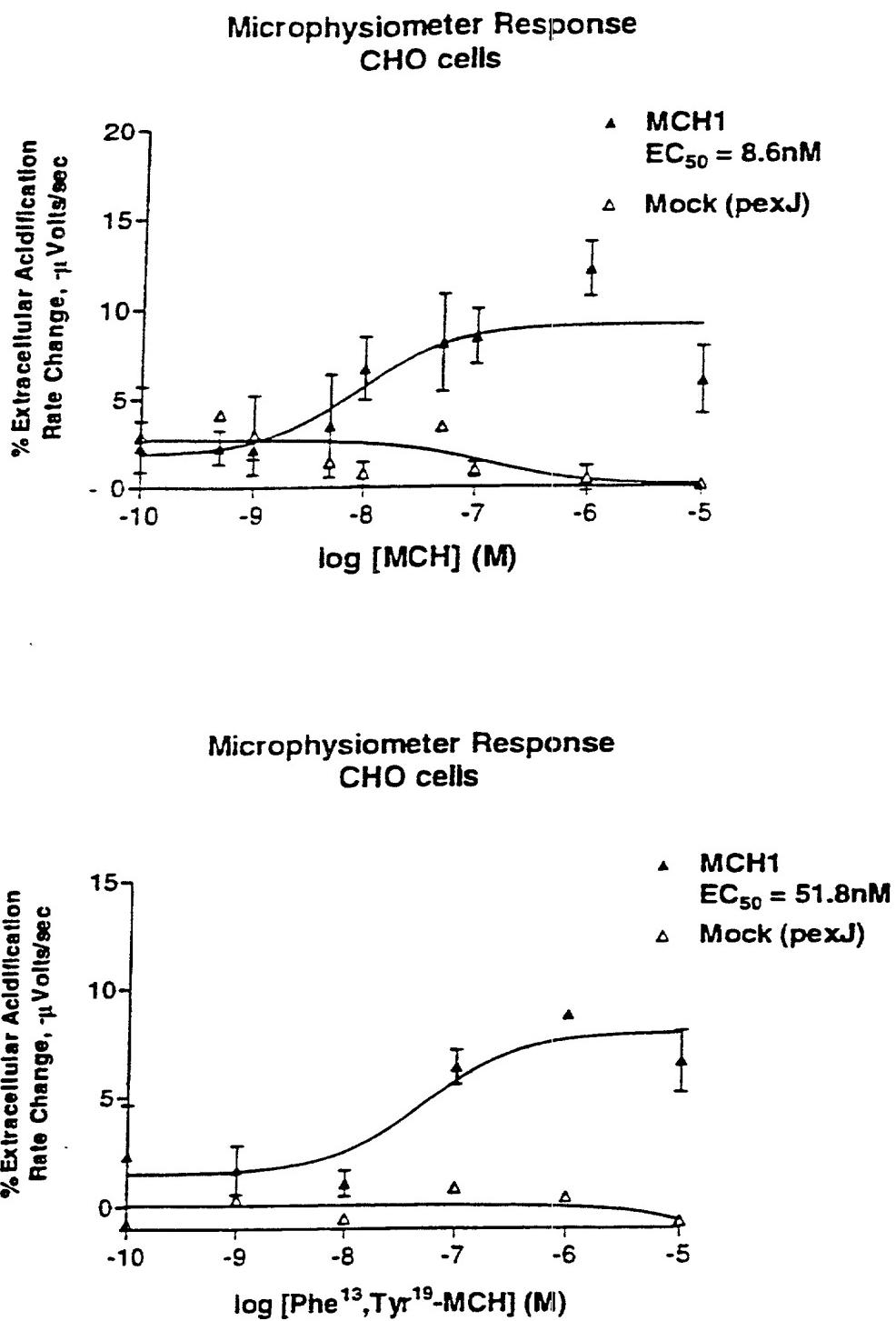


FIGURE 9

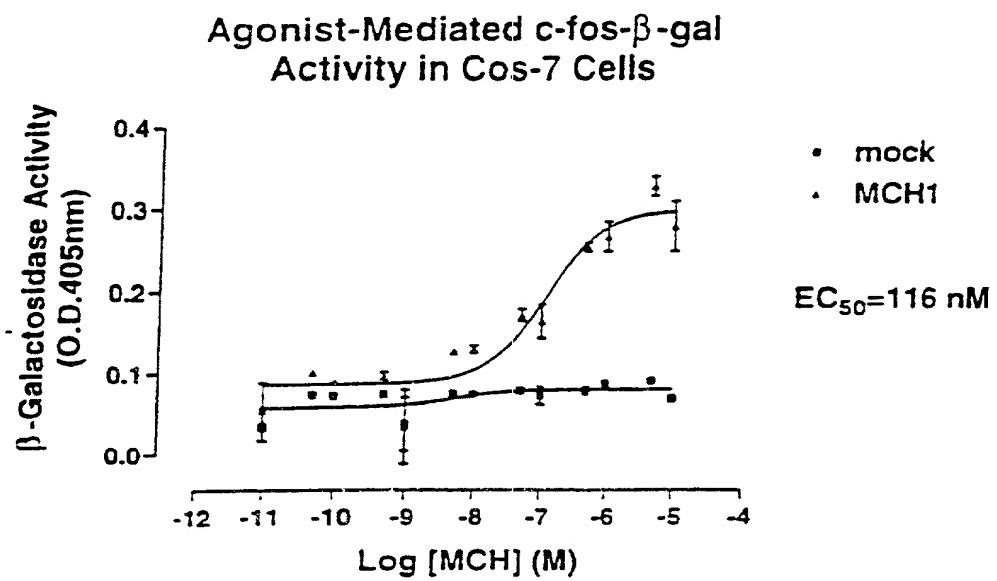
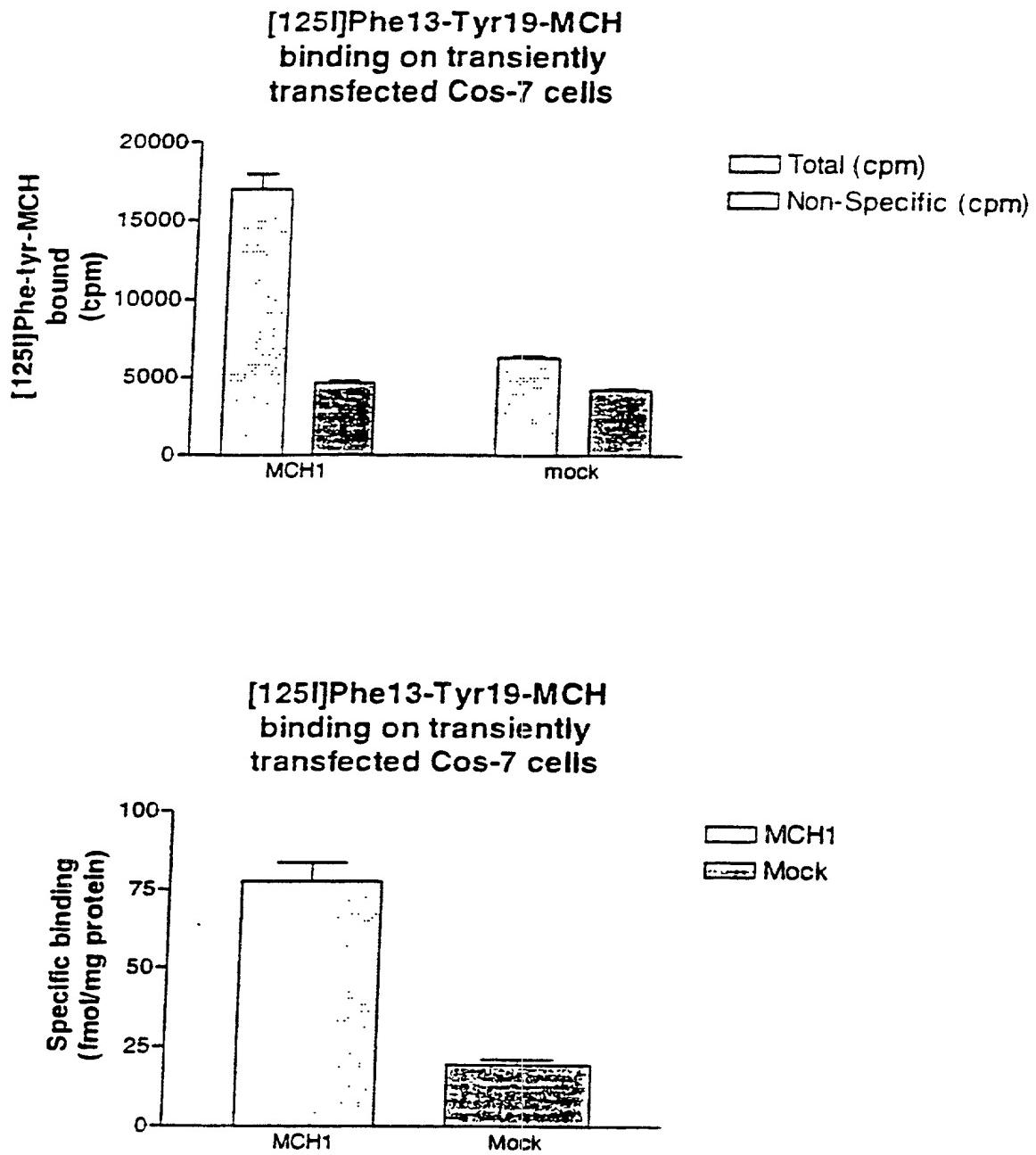
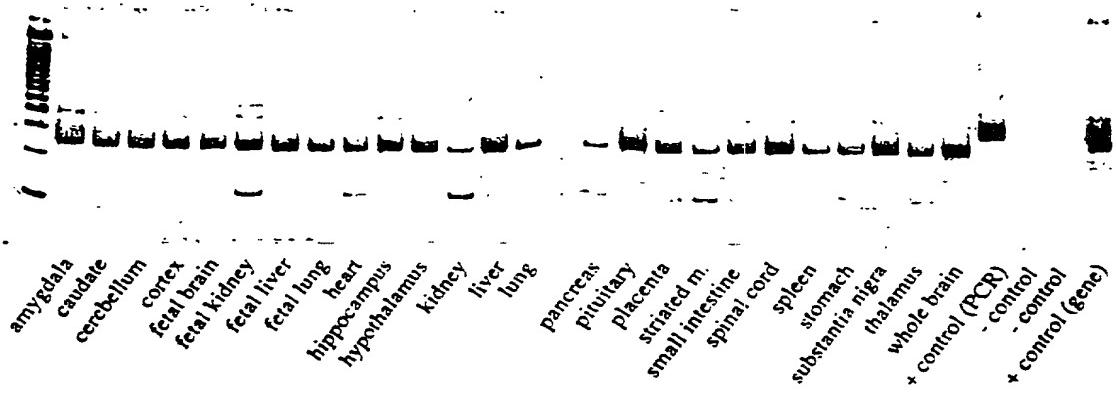


FIGURE 10



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FIGURE 11



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Figure 12

	1				
TL231	<b>MSVGAMKKGV</b>	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ	40
R106	<b>MSVGAMKKGV</b>	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ	
R114	<b>MSVGAaKKGV</b>	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ	
BO120	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~

	41				
TL231	GGRRWRLPQP	AWVEGSSARL	WEQATGTGWM	DLEASLLPTG	80
R106	GGRRWRLPQP	AWVEGSSARL	WEQATGTGWa	DLEASLLPTG	
R114	GGRRWRLPQP	AWVEGSSARL	WEQATGTGWa	DLEASLLPTG	
BO120	~~~~~	~~~~~	~~~~~M	DLEASLLPTG	

	81	100			
TL231	PNASNTSDGP	DNLTSAGSPP...			
R106	PNASNTSDGP	DNLTSAGSPP...			
R114	PNASNTSDGP	DNLTSAGSPP...			
BO120	PNASNTSDGP	DNLTSAGSPP...			

1	M S V G A M K K G V G R A V G L G G G S	20
21	G C Q A T E E D P L P D C G A C A P G Q	40
41	G G R R W R L P Q P A W V E G S S A R L	60
61	W E Q A T G T G W A D L E A S L L P T G	80
81	P N A S N T S D G P D N L T S A G S P P	100
101	R T G S I S Y I N I I M P S V F G T I C	120
121	L L G I I G N S T V I F A V V K K S K L	140
141	H W C N N V P D I F I I N L S V V D L L	160
161	F L L G M P F M I H Q L M G N G V W H F	180
181	G E T M C T L I T A M D A N S Q F T S T	200
201	Y I L T A M A I D R Y L A T V H P I S S	220
221	T K F R K P S V A T L V I C L L W A L S	240
241	F I S I T P V W L Y A R L I P F P G G A	260
261	V G C G I R L P N P D T D L Y W F T L Y	280
281	Q F F L A F A L P F V V I T A A Y V R I	300
301	L Q R M T S S V A P A S Q R S I R L R T	320
321	K R V T R T A I A I C L V F F V C W A P	340
341	Y Y V L Q L T Q L S I S R P T L T F V Y	360
361	L Y N A A I S L G Y A N S C L N P F V Y	380
381	I V L C E T F R K R L V L S V K P A A Q	400
401	G Q L R A V S N A Q T A D E E R T E S K	420
421	G T	422

1	M S V G A A K K G V G R A V G L G G G S	20
21	G C Q A T E E D P L P D C G A C A P G Q	40
41	G G R R W R L P Q P A W V E G S S A R L	60
61	W E Q A T G T G W A D L E A S L L P T G	80
81	P N A S N T S D G P D N L T S A G S P P	100
101	R T G S I S Y I N I I M P S V F G T I C	120
121	L L G I I G N S T V I F A V V V K K S K L	140
141	H W C N N V P D I F I I N L S V V D L L	160
161	F L L G M P F M I H Q L M G N G V W H F	180
181	G E T M C T L I T A M D A N S Q F T S T	200
201	Y I L T A M A I D R Y L A T V H P I S S	220
221	T K F R K P S V A T L V I C L L W A L S	240
241	F I S I T P V W L Y A R L I P F P G G A	260
261	V G C G I R L P N P D T D L Y W F T L Y	280
281	Q F F L A F A L P F V V I T A A Y V R I	300
301	L Q R M T S S V A P A S Q R S I R L R T	320
321	K R V T R T A I A I C L V F F V C W A P	340
341	Y Y V L Q L T Q L S I S R P T L T F V Y	360
361	L Y N A A I S L G Y A N S C L N P F V Y	380
381	I V L C E T F R K R L V L S V K P A A Q	400
401	G Q L R A V S N A Q T A D E E R T E S K	420
421	G T	422

1	M D L E A S L L P T G P N A S N T S D G	20
21	P D N L T S A G S P P R T G S I S Y I N	40
41	I I M P S V F G T I C L L G I I G N S T	60
61	V I F A V V K K S K L H W C N N V P D I	80
81	F I I N L S V V D L L F L L G M P F M I	100
101	H Q L M G N G V W H F G E T M C T L I T	120
121	A M D A N S Q F T S T Y I L T A M A I D	140
141	R Y L A T V H P I S S T K F R K P S V A	160
161	T L V I C L L W A L S F I S I T P V W L	180
181	Y A R L I P F P G G A V G C G I R L P N	200
201	P D T D L Y W F T L Y Q F F L A F A L P	220
221	F V V I T A A Y V R I L Q R M T S S V A	240
241	P A S Q R S I R L R T K R V T R T A I A	260
261	I C L V F F V C W A P Y Y V L Q L T Q L	280
281	S I S R P T L T F V Y L Y N A A I S L G	300
301	Y A N S C L N P F V Y I V L C E T F R K	320
321	R L V L S V K P A A Q G Q L R A V S N A	340
341	Q T A D E E R T E S K G T	353